



Steroidogenesiscorrected.ST25.txt  
SEQUENCE LISTING

<110> Stocco, Douglas M  
Clark, Barbara J  
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<130> 18491.40  
<140> US 09/612,894  
<141> 2000-07-10  
<160> 19  
<170> PatentIn version 3.2  
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RECEIVED  
OCT 01 2003  
TECH CENTER 1600/2900

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Thr Leu Tyr Ser Asp Gln Glu Leu Ser Tyr Ile Gln Gln Gly Glu Val  
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Pro Asp Val Gly Lys Val Phe Arg Leu Glu Val Val Val Asp Gln Pro  
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Glu Trp Asn Pro Asn Val Lys Glu Ile Lys Val Leu Gln Arg Ile Gly  
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Lys Asp Thr Val Ile Thr His Glu Leu Ala Ala Ala Ala Gly Asn  
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Leu Val Gly Pro Arg Asp Phe Val Ser Val Arg Cys Thr Lys Arg Arg  
 180 185 190

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Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met  
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Pro Glu Gln Ser Gly Val Ile Arg Ala Glu His Gly Pro Thr Cys Met  
210 215 220

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Glu Thr Leu Tyr Ser Asp Gln Glu Leu Ala Tyr Leu Gln Gln Gly Glu  
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Glu Ala Met Gln Lys Ala Leu Gly Ile Leu Ser Asn Gln Glu Gly Trp  
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Lys Lys Glu Ser Gln Gln Asp Asn Gly Asp Lys Val Met Ser Lys Val  
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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Stocco, Douglas M.  
Clark, Barbara J.

(ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATION OF  
STEROIDOGENESIS

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Akin, Gump, Strauss, Hauer & Feld, L.L.P.  
(B) STREET: 1900 Frost Bank Plaza, 816 Congress Avenue  
(C) CITY: Austin  
(D) STATE: TX  
(E) COUNTRY: U.S.A.  
(F) ZIP: 78701

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE:  
(B) COMPUTER:  
(C) OPERATING SYSTEM:  
(D) SOFTWARE:

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Unknown  
(B) FILING DATE: Concurrently Herewith  
(C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mayfield, Denise L.  
(B) REGISTRATION NUMBER: 33,732  
(C) REFERENCE/DOCKET NUMBER: 043375.0006/DLM

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 512/499-6200

(B) TELEFAX: 512/499-6290

5 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1466 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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25	CTGCTTGTTT CTCAACTGGA AGCAACACTC TATAGTGACC AGGAGCTGTC CTACATCCAG	300
	CAGGGAGAGG TGGCTATGCA GAAGGCCTTG GGCATACTCA ACAACCAGGA AGGCTGGAAG	360
	AAGGAAAGCC AGCAGGAGAA CGGGGACGAA GTGCTAAGTA AGATGGTGCC AGATGTGGGC	420
30	AAGGTGTTTC GCTTGGAGGT GGTGGTAGAC CAGCCCATGG ACAGACTCTA TGAAGAACTT	480
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5 GCTGAACACG GCCCCACCTG CATGGTGCTT CATCCACTGG CTGGAAGTCC CTCCAAGACT 780

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

10	Met	Phe	Leu	Ala	Thr	Phe	Lys	Leu	Cys	Ala	Gly	Ser	Ser	Tyr	Arg	His	
	1				5						10					15	
	Met	Arg	Asn	Met	Lys	Gly	Leu	Arg	His	Gln	Ala	Val	Leu	Ala	Ile	Gly	
				20				25						30			
15	Gln	Glu	Leu	Asn	Trp	Arg	Ala	Leu	Gly	Asp	Ser	Ser	Pro	Gly	Trp	Met	
			35					40						45			
	Gly	Gln	Val	Arg	Arg	Arg	Ser	Ser	Leu	Leu	Gly	Ser	Gln	Leu	Glu	Ala	
			50					55						60			
20	Thr	Leu	Tyr	Ser	Asp	Gln	Glu	Leu	Ser	Tyr	Ile	Gln	Gln	Gly	Glu	Val	
	65					70					75					80	
	Ala	Met	Gln	Lys	Ala	Leu	Gly	Ile	Leu	Asn	Asn	Gln	Glu	Gly	Trp	Lys	
25				85						90						95	
	Lys	Glu	Ser	Gln	Gln	Glu	Asn	Gly	Asp	Glu	Val	Leu	Ser	Lys	Met	Val	
				100					105						110		
30	Pro	Asp	Val	Gly	Lys	Val	Phe	Arg	Leu	Glu	Val	Val	Val	Asp	Gln	Pro	
			115						120						125		
	Met	Asp	Arg	Leu	Tyr	Glu	Glu	Leu	Val	Asp	Arg	Met	Glu	Ala	Met	Gly	
35			130					135						140			

	Glu Trp Asn Pro Asn Val Lys Glu Ile Lys Val Leu Gln Arg Ile Gly	
	145	150 155 160
5	Lys Asp Thr Val Ile Thr His Glu Leu Ala Ala Ala Ala Gly Asn	
	165	170 175
	Leu Val Gly Pro Arg Asp Phe Val Ser Val Arg Cys Thr Lys Arg Arg	
	180	185 190
10	Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met	
	195	200 205
	Pro Glu Gln Ser Gly Val Ile Arg Ala Glu His Gly Pro Thr Cys Met	
	210	215 220
15	Val Leu His Pro Leu Ala Gly Ser Pro Ser Lys Thr Lys Leu Thr Trp	
	225	230 235 240
	Leu Leu Ser Ile Asp Leu Lys Gly Trp Leu Pro Lys Thr Ile Ile Asn	
20	245	250 255
	Gln Val Leu Ser Gln Thr Gln Ile Glu Phe Ala Asn His Leu Arg Lys	
	260	265 270
25	Arg Leu Glu Ala Ser Pro Ala Ser Glu Ala Gln Cys	
	275	280

(2) INFORMATION FOR SEQ ID NO:3:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

35



(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5       Ala Glu His Gly Pro Thr Cys Met Val Leu His Pro Leu Ala  
      1                   5                   10

(2) INFORMATION FOR SEQ ID NO:4:

10       (i) SEQUENCE CHARACTERISTICS:  
          (A) LENGTH: 12 amino acids  
          (B) TYPE: amino acid  
          (C) STRANDEDNESS: single  
          (D) TOPOLOGY: linear

15       (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

20       Ala Leu Gly Ile Leu Asn Asn Gln Glu Gly Trp Lys  
      1                   5                   10

(2) INFORMATION FOR SEQ ID NO:5:

25       (i) SEQUENCE CHARACTERISTICS:  
          (A) LENGTH: 19 amino acids  
          (B) TYPE: amino acid  
          (C) STRANDEDNESS: single  
30       (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

35

Gly Ser Thr Cys Val Leu Ala Gly Met Ala Thr His Phe Gly Glu Met

1 5 10 15

Pro Glu Gln

5

(2) INFORMATION FOR SEQ ID NO:6:

- 10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

20 Asn Gln Glu Gly Trp Lys

1 5

(2) INFORMATION FOR SEQ ID NO:7:

25

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

35

Ala Glu His Gly Pro Thr Cys Met Val

1

5

5 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ile Leu Asn Asn Gln Glu Gly Trp Lys Lys Glu

1

5

10

20 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

30

(ix) FEATURE:

(A) NAME/KEY: modified\_base

(B) LOCATION: one-of(3, 12, 15, 18)

(D) OTHER INFORMATION: /mod\_base= OTHER

35 /note= "N = (A or C or G or T/U) or (unknown or other)"

(ix) FEATURE:

(A) NAME/KEY: modified\_base

(B) LOCATION: 6

(D) OTHER INFORMATION: /mod\_base= OTHER

5 /note= "R = A or G"

(ix) FEATURE:

(A) NAME/KEY: modified\_base

(B) LOCATION: one-of(9, 21)

10 (D) OTHER INFORMATION: /mod\_base= OTHER

/note= "Y = C or T/U"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

15

GCNGARCAYG GNCCNACNTG YATGG

25

(2) INFORMATION FOR SEQ ID NO:10:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(ix) FEATURE:

30

(A) NAME/KEY: modified\_base

(B) LOCATION: one-of(5, 17)

(D) OTHER INFORMATION: /mod\_base= OTHER

/note= "R = A or G"

35

(ix) FEATURE:

(A) NAME/KEY: modified\_base  
(B) LOCATION: one-of(8, 11, 14, 23)  
(D) OTHER INFORMATION: /mod\_base= OTHER  
/note= "N = (A or C or G or T/U) or (unknown or other)"

5

(ix) FEATURE:

(A) NAME/KEY: modified\_base  
(B) LOCATION: 20  
(D) OTHER INFORMATION: /mod\_base= OTHER

10

/note= "Y = C or T/U"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCATRCANGT NGGNC CRTGY TCNGC

25

15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "DNA"

(ix) FEATURE:

(A) NAME/KEY: modified\_base

30

(B) LOCATION: 3

(D) OTHER INFORMATION: /mod\_base= OTHER

/note= "Y = C or T/U"

(ix) FEATURE:

35

(A) NAME/KEY: modified\_base

(B) LOCATION: one-of(6, 9)

(D) OTHER INFORMATION: /mod\_base= OTHER

/note= "R = A or G"

5 (ix) FEATURE:

(A) NAME/KEY: modified\_base

(B) LOCATION: 12

(D) OTHER INFORMATION: /mod\_base= OTHER

/note= "N = (A or C or G or T/U) or (unknown or other)"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAYCARCARG GNTGGAA

17

15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

20

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

25

(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCCANCCYT CYTGRTT

17

30

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 401 base pairs

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10	AACCAGGAAG GCTGGAAGAA GGAAAGCCAG CAGGAGAACG GGGACGAAGT GCTAAGTAAG	60
	ATGGTGCCAG ATGTGGGCAA GGTGTTTCGC TTGGAGGTGG TGGTAGACCA GCCCATGGAC	120
	AGACTCTATG AAGAACTTGT GGACCGCATG GAGGCCATGG GAGAGTGGAA CCCAAATGTC	180
15	AAGGAGATCA AGGTCCTGCA GAGGATTGGA AAAGACACGG TCATCACTCA TGAGCTGGCT	240
	GCGGCGGCAG CAGGCAACCT GGTGGGGCCT CGAGACTTCG TGAGCGTGCG CTGTACCAAG	300
20	CGCAGAGGTT CCACCTGTGT GCTGGCAGGC ATGGCCACAC ATTTTGGGGA GATGCCGGAG	360
	CAGAGTGGTG TCATCAGAGC TGAACACGGC CCCACCTGCA T	401

25 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1466 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "RNA"

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

	GUCGACCCAC GCGUCCGCUC AGGACCUUGA AAGGCUCAGG AAGAACAACC CUUGAGCACC	60
5	UCAGCACUCA GCAUGUUCU CGCUACGUUC AAGCUGUGUG CUGGAAGCUC CUAUAGACAU	120
	AUGCGGAAUA UGAAAGGAUU AAGGCACCAA GCUGUGCUGG CCAUUGGCCA AGAGCUCAAC	180
	UGGAGAGCAC UGGGGGAUUC CAGUCCCGGG UGGAUGGGUC AAGUUCGACG UCGGAGCUCU	240
10	CUGCUUGGUU CUCAACUGGA AGCAACACUC UAUAGUGACC AGGAGCUGUC CUACAUCAG	300
	CAGGGAGAGG UGGCUAUGCA GAAGGCCUUG GGCAUACUCA ACAACCAGGA AGGCUGGAAG	360
15	AAGGAAAGCC AGCAGGAGAA CGGGGACGAA GUGCUAAGUA AGAUGGUGCC AGAUGUGGGC	420
	AAGGUGUUUC GCUUGGAGGU GGUGGUAGAC CAGCCCAUGG ACAGACUCUA UGAAGAACUU	480
	GUGGACCGCA UGGAGGCCAU GGGAGAGUGG AACCCAAUG UCAAGGAGAU CAAGGUCCUG	540
20	CAGAGGAUUG GAAAAGACAC GGUCAUCACU CAUGAGCUGG CUGCGGCGGC AGCAGGCAAC	600
	CUGGUGGGGC CUCGAGACUU CGUGAGCGUG CGCUGUACCA AGCGCAGAGG UUCCACCUGU	660
25	GUGCUGGCAG GCAUGGCCAC ACAUUUUGGG GAGAUGCCGG AGCAGAGUGG UGUCAUCAGA	720
	GCUGAACACG GCCCCACCUG CAUGGUGCUU CAUCCACUGG CUGGAAGUCC CUCCAAGACU	780
	AAACUCACUU GGCUGCUCAG UAUUGACCUG AAGGGGUGGC UGCCGAAGAC AAUCAUCAAC	840
30	CAGGUCCUAU CGCAGACCCA GAUAGAGUUC GCCAACCACC UGCGCAAGCG CCUGGAAGCC	900
	AGCCUGCCU CUGAGGCCCA GUGUUAAGGA CUGUCCACCA CAUUGACCUG CAAAUCAUUG	960
35	GAAGCUCUCA CAGGAAGCCU GCAAGUCUGU CCAUCUUCAG CUAACAGCAU CGGGAGGGGU	1020



	GGUAGUCAGG AGACACUAGG ACUGACUGGU AAAAUCAGGA UCAGCAAAAU AGAAAUGAGG	1080
	CUUAGAAUAA AAGUUCUCUA GUGUCUCCCA CUGCAUAGCU GUGAAGGCUA AGGGAUAAGU	1140
5	AGCUAUGAAA CCUUUCAUCU AGGCUUGUAU AUGCUGACCU AAAAGACACC AGCAGCUACG	1200
	AACAGGGGAU GCUAAGGAUC GGGAACTUGU GUCUUACCAG CUCCAAAUGU CACUACCUGA	1260
	AGGCAGUGUG CACACAAAGC AAGGUCUUGC CUAGGAAACU CUGUAAAAGU UCUCUCUGU	1320
10	AAAAGGCCAG AACUUGAUG AAACUACCUA CAAAGGGCCU UCCAGAGUA UCCAACUUU	1380
	UCUCUGAGGA GAAUGAAAC CAUCAUGUG CCGACUCCC UACUAAUCCC AUGACAAUAA	1440
15	AGAACAUACA UAAAAAAAAA AAAAAA	1466

(2) INFORMATION FOR SEQ ID NO:15:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:
- (B) TYPE:
- (C) STRANDEDNESS:
- (D) TOPOLOGY:

25 (ii) MOLECULE TYPE:

(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:15:

30

267	GTGGATTAAC CAGGTTCCGC GCGGAGCTC TCTACTCGGT TCTCGGCTGG AAGAGACTCT	326
327	CTACAGTGAC CAGGAGCTGG CCTATCTCCA GCAGGGGGAG GAGGCCATGC AGAAGGCCTT	386
387	GGGCATCCTT AGCAACCAAG AGGGCTGGAA GAAGGAGAGT CAGCAGGACA ATGGGGACAA	446
447	AGTGATGAGT AAAGTGGTCC CAGATGTGGG CAAGGTGTTC CGGCTGGAGG TCGTGGTGGA	506
35	507 CCAGCCCATG GAGAGGCTCT ATGAAGAGCT CGTGGAGCGC ATGGAAGCAA TGGGGGAGTG	566

567 GAACCCCAAT GTCAAGGAGA TCAAGGTCCT GCAGAAGATC GGAAAAGATA CATTATTAC 626  
 627 TCACGAGCTG GCTGCCGAGG CAGCAGGAAA CCTGGTGGGG CCCCCTGACT TTGTGAGCGT 686  
 687 GCGCTGTGCC AAGCGCCGAG GCTCCACCTG TGTGCTGGCT GGCATGGACA CAGACTTCGG 746  
 747 GAACATGCCT GAGCAGAAGG GTGTCATCAG GGCGGAGCAC GGTCCCCTT GCATGGTGCT 806  
 5 807 TCACCCGTTG GCTGGAAGTC CCTCTAAGAC CAAACTTACG TGGCTACTCA GCATCGACCT 866  
 867 CAAGGGGTGG CTGCCAAGA GCATCATCAA CCAGGTCCTG TCCCAGACCC AGGTGGATTT 926  
 927 TGCCAACCAC CTGCGCAAGC GCCTGGAGTC CCACCTGCC TCTGAAGCCA GGTGTTGAAG 986  
 987 AC 988

10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH:
- (B) TYPE:
- (C) STRANDEDNESS:
- (D) TOPOLOGY:

(ii) MOLECULE TYPE:

20

- (A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:16:

25

127 ATGCTGCTAG CGACATTCAA GCTGTGCGCT GGGAGCTCCT ACAGACACAT GCGCAACATG 186  
 187 AAGGGGCTGA GGCAACAGGC TGTGATGGCC ATCAGCCAGG AGCTGAACCG GAGGGCCCTG 246  
 247 GGGGGCCCCA CCCC 260

(2) INFORMATION FOR SEQ ID NO:17:

30

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH:
- (B) TYPE:
- (C) STRANDEDNESS:
- (D) TOPOLOGY:

(ii) MOLECULE TYPE:

(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:17:

5

1051 ACTGGAAGCC TGCAAGTCT 1069

(2) INFORMATION FOR SEQ ID NO:18:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

15

(D) TOPOLOGY:

(ii) MOLECULE TYPE:

(A) DESCRIPTION:

20

SEQUENCE DESCRIPTION: SEQ ID NO:18:

1	MLLATFKLCA GSSYRHMNRNM KGLRQQAVMA ISQELNRRAL GGTPSTWIN	50
51	QVRRRSSLLG SRLEETLYSD QELAYLQQGE EAMQKALGIL SNQEGWKES	100
101	QQDNGDKVMS KVPDVGVKF RLEVVDQPM ERLYEELVER MEAMGEWNP	150
25	151 VKEIKVLQKI GKDTFITHL AAEAAGNLVG PRDFVSVRCA KRRGSTCVLA	200
	201 GMATDFGNMP EQKGVIRAEH GPTCMVLHPL AGSPSKTKLT WLLSIDLKGW	250
	251 LPKSIINQVL SQTQVDFANHL RKRLESHPA SEARC	285

(2) INFORMATION FOR SEQ ID NO:19:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:

(B) TYPE:

(C) STRANDEDNESS:

35

(D) TOPOLOGY:

(ii) MOLECULE TYPE:

(A) DESCRIPTION:

SEQUENCE DESCRIPTION: SEQ ID NO:19:

5

agaacaccag gtccaggctg cagctgcggg actcagaggc gaacgttgag gggctcagga 60  
aggacgaaga accacccttg agagaagagg cagcagcagc gcggcagcag cagcggcagc 120  
gacccccacca ctgccacatt tgccaggaaa caATGCTGCT AGCGACATTC AAGCTGTGCG 180  
CTGGGAGCTC CTACAGACAC ATGCGCAACA TGAAGGGGCT GAGGCAACAG GCTGTGATGG 240  
10 CCATCAGCCA GGAGCTGAAC CGGAGGGCCC TGGGGGGCCC CACCCCTAGC ACGTGGATTA 300  
ACCAGGTTTC GCGGCGGAGC TCTCTACTCG GTTCTCGGCT GGAAGAGACT CTCTACAGTG 360  
ACCAGGAGCT GGCCTATCTC CAGCAGGGGG AGGAGGCCAT GCAGAAAGGCC TTGGGCATCC 420  
TTAGCAACCA AGAGGGCTGG AAGAAGGAGA GTCAGCAGGA CAATGGGGAC AAAGTGATGA 480  
GTAAAGTGGT CCCAGATGTG GGCAAGGTGT TCCGGCTGGA GGTCGTGGTG GACCAGCCCA 540  
15 TGGAGAGGCT CTATGAAGAG CTCGTGGAGC GCATGGAAGC AATGGGGGAG TGAACCCCA 600  
ATGTCAAGGA GATCAAGGTC CTGCAGAAGA TCGGAAAAGA TACATTCATT ACTCACGAGC 660  
TGGCTGCCGA GGCAGCAGGA AACCTGGTGG GGCCCCGTGA CTTTGTGAGC GTGCGCTGTG 720  
CCAAGCGCCG AGGCTCCACC TGTGTGCTGG CTGGCATGGC CACAGACTTC GGAACATGC 780  
CTGAGCAGAA GGGTGTGATC AGGGCGGAGC ACGGTCCAC TTGCATGGTG CTTACCCCGT 840  
20 TGGCTGGAAG TCCCTCTAAG ACCAACTTA CGTGGCTACT CAGCATCGAC CTCAAGGGGT 900  
GGCTGCCCAA GAGCATCATC AACCAGGTCC TGTCACAGAC CCAGGTGGAT TTTGCCAACC 960  
ACCTGCGCAA GCGCCTGGAG TCCCACCCTG CCTCTGAAGC CAGGTGTTGA agaccagcct 1020  
gctgttccca actgtgccca gctgcactgg tacacacgct catcaggaga atccctactg 1080  
gaagcctgca agtctaagat ctccatctgg tgacagtggg atgggtgggg ttcgtgttta 1140  
25 gagtatgaca ctaggattca gattggtgaa agtttttagt accaagaaaa cagggatgag 1200  
ctcttggatt aaaaggtaac ttcattcact gattagctat gacatgaggg ttcaggcccc 1260  
ctaaaaataa ttgtaaaact ttttttctgg gcccttatgt acccacctaa aaccatcttt 1320  
aaaatgctag tggctgatat ggggtgtggg gatgctaacc acagggcctg agaagtcttg 1380  
ctttatgggc tcaagaatgc catgcgctgg cagtacatgt gcacaaagca gaatctcaga 1440  
30 ggggtctctg cagccctctg ctctcccg ccgctgcaca gcaacaccac agaacaagca 1500  
gcacccca gtgggtgcct tccagaaata tagtccaagc tttctctgtg gaaaaagaca 1560  
aaactcatta gtagacatgt ttcctattg ctttcatagg caccagtcag aataaagaat 1620  
cataattcac acaaaaaaaaa a 1641